



# UNITED STATES PATENT AND TRADEMARK OFFICE

UNITED STATES DEPARTMENT OF COMMERCE  
United States Patent and Trademark Office  
Address: COMMISSIONER FOR PATENTS  
P.O. Box 1450  
Alexandria, Virginia 22313-1450  
www.uspto.gov

11

APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/990,437	11/16/2001	Avi J. Ashkenazi	P2730PIC49	2360

35489 7590 11/09/2004

HELLER EHRMAN WHITE & MCAULIFFE LLP  
275 MIDDLEFIELD ROAD  
MENLO PARK, CO 94025-3506

EXAMINER
----------

KAUFMAN, CLAIRE M

ART UNIT	PAPER NUMBER
----------	--------------

1646

DATE MAILED: 11/09/2004

Please find below and/or attached an Office communication concerning this application or proceeding.

### Office Action Summary

**Application No.**

09/990,437

**Applicant(s)**

ASHKENAZI ET AL.

**Examiner**

Claire M Kaufman

**Art Unit**

1646

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

#### Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

#### Status

- 1) ☒ Responsive to communication(s) filed on 20 August 2004.
- 2a) ☐ This action is **FINAL**. 2b) ☒ This action is non-final.
- 3) ☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

#### Disposition of Claims

- 4) ☒ Claim(s) 123-125, 129-131 and 135-138 is/are pending in the application.
- 4a) Of the above claim(s) \_\_\_\_\_ is/are withdrawn from consideration.
- 5) ☒ Claim(s) 131 is/are allowed.
- 6) ☐ Claim(s) 123-125 and 135-138 is/are rejected.
- 7) ☐ Claim(s) 129 and 130 is/are objected to.
- 8) ☐ Claim(s) \_\_\_\_\_ are subject to restriction and/or election requirement.

#### Application Papers

- 9) ☐ The specification is objected to by the Examiner.
- 10) ☐ The drawing(s) filed on \_\_\_\_\_ is/are: a) ☐ accepted or b) ☐ objected to by the Examiner.  
Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).  
Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).
- 11) ☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

#### Priority under 35 U.S.C. § 119

- 12) ☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).
- a) ☐ All b) ☐ Some \* c) ☐ None of:
1. ☐ Certified copies of the priority documents have been received.
  2. ☐ Certified copies of the priority documents have been received in Application No. \_\_\_\_\_.
  3. ☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

\* See the attached detailed Office action for a list of the certified copies not received.

#### Attachment(s)

- |  |   |
|--|---|
| 1) <input type="checkbox"/> Notice of References Cited (PTO-892)   | 4) <input type="checkbox"/> Interview Summary (PTO-413)<br>Paper No(s)/Mail Date. _____ |
| 2) <input type="checkbox"/> Notice of Draftsperson's Patent Drawing Review (PTO-948)                                   | 5) <input type="checkbox"/> Notice of Informal Patent Application (PTO-152)             |
| 3) <input type="checkbox"/> Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08)<br>Paper No(s)/Mail Date _____ | 6) <input checked="" type="checkbox"/> Other: <u>Sequence Comparison</u> .              |

## **DETAILED ACTION**

### ***Response to Arguments***

The rejections of claims under 35 USC 112, second paragraph and first paragraph-written description, are withdrawn in view of the amendment to the claims or moot in view of cancellation of the claims. A new rejection appears below due to the amendment.

The rejections of claims under 35 USC 102 as anticipated by US 6,607,879 and 5,952,223 are withdrawn in view of the amendment to the claims. Neither of the cited US Patents or the discloses the full coding sequence of SEQ ID NO:32 or a nucleic acid at least 99% identical thereto. Note there is a new rejection under 35 USC 102.

### ***Claim Interpretation***

For claims drawn to "An isolated nucleic acid comprising a nucleic acid sequence" of SEQ ID NO:32 or encoding a polypeptide of SEQ ID NO:33 (Claim 124), the specification appears to intend that the nucleic acid and amino acid sequences are contiguous, but the isolated nucleic acid and polypeptide may include additional nucleic acid or amino acid sequence, respectively, on either end of said sequence (*e.g.*, p.304, lines 19-25). With this interpretation, the splice variant of GenBank AB011112.1 which encodes a polypeptide identical to SEQ ID NO:33 of the instant application with the exception of a 30 amino acid insert and is encoded by a nucleic acid identical to SEQ ID NO:32 with the exception of a 90 nucleotide insert, would not qualify as a nucleic acid comprising the nucleic acid sequence of SEQ ID NO:32 or encoding the polypeptide SEQ ID NO:33. For this reason, the GenBank reference is not being applied to claim 124. If Applicants feel this interpretation is in error, this should be stated in the response to this office action and will not preclude the next Office action from being made final since the issue was raised here.

This interpretation does not apply to isolated nucleic acids 99 % identical (or some other % identity) to SEQ ID NO:33, which allows gaps/inserts (see art rejection below).

### ***Claim Objections***

Claims 123-125 and 129 and 130 are objected to because of the following informalities: the SEQ ID NO: appears in parenthesis, which appears to be an advertent typographical error introduced by the amendment to the claims. Appropriate correction is required.

***Claim Rejections - 35 USC § 112***

The following is a quotation of the second paragraph of 35 U.S.C. 112:

The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

Claim 123 is rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

Claim 123 is dependent on cancelled claim 119, so the metes and bounds of the claim are not clear.

***Claim Rejections - 35 USC § 112***

The following is a quotation of the first paragraph of 35 U.S.C. 112:

The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

Claims 123-125 and 135-138 remain rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for the nucleic acid of SEQ ID NO:33 or a nucleic acid sequence at least 99% identical to SEQ ID NO:32 wherein said nucleic acid is amplified in squamous cell-type lung carcinomas, does not reasonably provide enablement for a 99% identical nucleic acid amplified in colon tumors or for a nucleic acid encoding a polypeptide of SEQ ID NO:33. The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to use the invention commensurate in scope with these claims and for the reasons set forth in the previous Office action and for the following reasons directed to the claims as amended.

The amendment to claim 123 introduces a functional limitation requiring said nucleic acid be amplified in squamous cell-type lung carcinomas (SqCCa) and colon tumors; however, while there is enablement for the amplification in squama cell-type lung carcinomas as indicated in the previous Office action on page 5, lines 15-18, with 5/11 SqCCa showing a  $\Delta Ct > 1.0$ , only 2/17 colon tumors had a  $\Delta Ct > 1.0$ , which is not a significant number on which to base enablement as a

Art Unit: 1646

colon tumor marker. Also, as stated in the previous Office action on page 5, lines 18-21, "Detection is predicated on structural relationship of the nucleic acid probe to nucleic acids) in the tumor tissue. One skilled in the art would not predict that detection would have the required sensitivity if the probe sequence differed from SEQ ID NO:33 such as the sequence of a degenerate nucleic acid or a hybridizing nucleic acid." Claim 124 is drawn to a nucleic acid encoding a polypeptide of SEQ ID NO:33, which because of degeneracy of the genetic code would not be enabled unless the nucleic acid had the sequence of SEQ ID NO:32.

Applicants argue that the amendment to the claims provides enablement. The argument has been fully considered, but is not persuasive. For the reasons set forth above and in the previous Office action, the amendments do not make the claims listed in the rejection above due to inclusion of amplification in colon tumors or to inclusion of degenerate encoding nucleic acids.

### ***Priority***

Additionally, Applicants' argument directed to priority are persuasive in that priority application 60/141,037 (06/23/99, *e.g.*, p. 161 line 20) does disclose the enabling gene amplification data also found in the instant application.

### ***Claim Rejections - 35 USC § 102***

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless –

(a) the invention was known or used by others in this country, or patented or described in a printed publication in this or a foreign country, before the invention thereof by the applicant for a patent.

Claim 123 is rejected under 35 U.S.C. 102(a) as being anticipated by GenBank AB011112.1.

GenBank AB011112.1 teaches a nucleic acid at least 99% identical to SEQ ID NO:32 of the instant application. See attached SEQUENCE COMPARISON GenBank AB011112.1.

Note that for the nucleic acid there are only 3 mismatches over 3504 nucleotides with the admittance of a gap. This leads to a >99% identity. The following definitions percent identity are from the specification:

Art Unit: 1646

"Percent (%) nucleic acid sequence identity" with respect to PRO-encoding nucleic acid sequences identified herein is defined as the percentage of nucleotides in a candidate sequence that are identical with the nucleotides in the PRO nucleic acid sequence of interest, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity. Alignment for purposes of determining." (p. 309, lines 1-4)

### ***Conclusion***

Claims 129-131 are allowable except for the objection to claims 129 and 130.

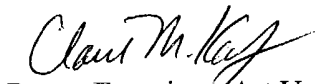
Any inquiry concerning this communication or earlier communications from the examiner should be directed to Claire M. Kaufman, whose telephone number is (571) 272-0873. Dr. Kaufman can generally be reached Monday, Tuesday and Thursday from 8:30AM to 2:30PM.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Brenda Brumback, can be reached at (571) 272-0961.

Any inquiry of a general nature or relating to the status of this application should be directed to the Group receptionist whose telephone number is (571) 272-1600.

Official papers filed by fax should be directed to (703) 872-9306. NOTE: If applicant *does* submit a paper by fax, the original signed copy should be retained by the applicant or applicant's representative. NO DUPLICATE COPIES SHOULD BE SUBMITTED so as to avoid the processing of duplicate papers in the Office. **Please** advise the examiner at the telephone number above before facsimile transmission.

Claire M. Kaufman, Ph.D.



Patent Examiner, Art Unit 1646

November 8, 2004

Art Unit: 1646

## SEQUENCE COMPARISON

LOCUS AB011112 6364 bp mRNA linear PRI 05-JUL-2002  
 DEFINITION Homo sapiens mRNA for KIAA0540 protein, partial cds.  
 ACCESSION AB011112  
 VERSION AB011112.3 GI:20521076  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1  
 AUTHORS Nagase,T., Ishikawa,K., Miyajima,N., Tanaka,A., Kotani,H.,  
 Nomura,N. and Ohara,O.  
 TITLE Prediction of the coding sequences of unidentified human genes. IX.  
 The complete sequences of 100 new cDNA clones from brain which can  
 code for large proteins in vitro  
 JOURNAL DNA Res. 5 (1), 31-39 (1998)  
 MEDLINE 98290545  
 PUBMED 9628581  
 REFERENCE 2 (bases 1 to 6364)  
 AUTHORS Ohara,O., Nagase,T. and Ishikawa,K.  
 TITLE Direct Submission  
 JOURNAL Submitted (13-FEB-1998) Osamu Ohara, Kazusa DNA Research Institute,  
 Laboratory of DNA Technology; Yana 1532-3, Kisarazu, Chiba  
 292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913,  
 Fax:+81-438-52-3914)  
 COMMENT On May 9, 2002 this sequence version replaced gi:6635198.  
 FEATURES  
 Location/Qualifiers  
 source 1..6364  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="pg00116"  
 /sex="male"  
 /tissue\_type="brain"  
 /clone\_lib="pBluescriptII SK plus"  
 /note="This sequence was replaced that of hg04185 cDNA as  
 a representative cDNA sequence for KIAA0540."  
 gene 1..6364  
 /gene="KIAA0540"  
 CDS <1..6128  
 /gene="KIAA0540"  
 /note="Start codon is not identified"  
 /codon\_start=3  
 /product="KIAA0540 protein"  
 /protein\_id="BAA25466.3"  
 /db\_xref="GI:20521077"  
 /translation="PMELRHLLRPRGLDSEPGGAEAGKARHAGAVIRTLSGMARHQG  
 PARALRYFDLTPSMAGIMVPPVQRWPGPGFTFHAWLCLHPMDTAPTAPTRPLQRKQL  
 YSFFTSSGSGFEAFFTAAGTLVVAVCTRKEYLTMSLPEVSFADSAWHCVAIVHVPGRR  
 PFSQNLVHVYKDGHLVKTAPLRCPSLSEPFSSCCIGSAGYRTTTTTTGLPTPPVPATL  
 AYTHPALTRSQSVPASTGLGWGSGLVAPLQEGSIDSTLAGTQDTRWGSPTSLEGELGA  
 VAIFHEALQATALRTLCTLGPNETAPFKPEGELHELSTRLLHYSPOACKNNICLDLS  
 PSHGLDGRLTGHRVETWDVKDVVNCVGGMGALLPLLERVAAQPKEAEAGPAETHDLVG  
 PELTSGHNTQGLVLP LKGSSEERMERNAVA AFLMLRNFLQGHMVNQESLVQCQGPAT

Query Match 96.6%; Score 2907.4; DB 9; Length 6364;  
Best Local Similarity 97.1%; Pred. No. 0;  
Matches 3008; Conservative 0; Mismatches 1; Indels 90; Gaps 1;

Qy	1	ATGTCCCAAGTTCGAAATGGACACGTATGCTAAGAGCCACGACCTTATGTCAGGTTTCTGG	60
Db	3027	ATGTCCCAAGTTCGAAATGGACACGTATGCTAAGAGCCACGACCTTATGTCAGGTTTCTGG	3086
Qy	61	AATGCCTGCTATGACATGCTTATGAGCAGTGCGGCCAGTGGGAGCGCGCCAG	120
Db	3087	AATGCCTGCTATGACATGCTTATGAGCAGTGCGGCCAGTGGGAGCGCGCCAG	3146
Qy	121	AGTCGTCGGGCCTTCCAGGAGCTGGTGCTGGAACCTGCGCAGAGGCGGGCGCGCCTGGAG	180
Db	3147	AGTCGTCGGGCCTTCCAGGAGCTGGTGCTGGAACCTGCGCAGAGGCGGGCGCGCCTGGAG	3206
Qy	181	GGGCTACGCTACACGGCAGTGCTGAAGCAGCAGGCAACGCAGCACTCCATGGCCCTGCTG	240
Db	3207	GGGCTACGCTACACGGCAGTGCTGAAGCAGCAGGCAACGCAGCACTCCATGGCCCTGCTG	3266
Qy	241	CACTGGGGGGCGCTGTGGCGCCAGCTCGCCAGCCCATGTGGGGCCTGGGCGCTGAGGGAC	300
Db	3267	CACTGGGGGGCGCTGTGGCGCCAGCTCGCCAGCCCATGTGGGGCCTGGGCGCTGAGGGAC	3326



Qy	301	ACTCCCATCCCCCGCTGGAAACTGTCCAGCGCCGAGACATATTACGCATGCGTCTGAAG	360
Db	3327	ACTCCCATCCCCCGCTGGAAACTGTCCAGCGCCGAGACATATTACGCATGCGTCTGAAG	3386
Qy	361	CTGGTGCCCAACCATCACTTCGACCCTCACCTGGAAGCCAGCGCTCTCCGAGACAATCTG	420
Db	3387	CTGGTGCCCAACCATCACTTCGACCCTCACCTGGAAGCCAGCGCTCTCCGAGACAATCTG	3446
Qy	421	GGTGAGGTTCCCCTGACACCCACCGAGGAGGCCTCACTGCCTCTGGCAGTGACCAAAGAG	480
Db	3447	GGTGAGGTTCCCCTGACACCCACCGAGGAGGCCTCACTGCCTCTGGCAGTGACCAAAGAG	3506
Qy	481	GCCAAAGTGAGCACCCCCACCCGAGTTGCTGCAGGAGGACCAGCTCGGCGAGGACGAGCTG	540
Db	3507	GCCAAAGTGAGCACCCCCACCCGAGTTGCTGCAGGAGGACCAGCTCGGCGAGGACGAGCTG	3566
Qy	541	GCTGAGCTGGAGACCCCCGATGGAGGCAGCAGAACTGGATGAGCAGCGTGAGAAGCTGGTG	600
Db	3567	GCTGAGCTGGAGACCCCCGATGGAGGCAGCAGAACTGGATGAGCAGCGTGAGAAGCTGGTG	3626
Qy	601	CTGTCGCGCCGAGTGCCAGCTGGTGACGGTAGTGGCCGTGGTCCCAGGGCTGCTGGAGGTC	660
Db	3627	CTGTCGCGCCGAGTGCCAGCTGGTGACGGTAGTGGCCGTGGTCCCAGGGCTGCTGGAGGTC	3686
Qy	661	ACCACACAGAATGTATACTTCTACGATGGCAGCACTGAGCGCGTGGAACCGAGGAGGGC	720
Db	3687	ACCACACAGAATGTATACTTCTACGATGGCAGCACTGAGCGCGTGGAACCGAGGAGGGC	3746
Qy	721	ATCGGCTATGATTTCCGGCGCCCACTGGCCCAGCTGCGTGAGGTCCACCTGCGGCGTTTC	780
Db	3747	ATCGGCTATGATTTCCGGCGCCCACTGGCCCAGCTGCGTGAGGTCCACCTGCGGCGTTTC	3806
Qy	781	AACCTGCGCCGTTTCAGCACTTGAGCTCTTCTTTATCGATCAGGCCAACTACTTCCTCAAC	840
Db	3807	AACCTGCGCCGTTTCAGCACTTGAGCTCTTCTTTATCGATCAGGCCAACTACTTCCTCAAC	3866
Qy	841	TTCCCATGCAAGGTGGGCACGACCCAGTCTCATCTCCTAGCCAGACTCCGAGACCCAG	900
Db	3867	TTCCCATGCAAGGTGGGCACGACCCAGTCTCATCTCCTAGCCAGACTCCGAGACCCAG	3926
Qy	901	CCTGGCCCCATCCACCCCATACCCAGGTACGGAACCAGGTGTACTCGTGGCTCCTGCGC	960
Db	3927	CCTGGCCCCATCCACCCCATACCCAGGTACGGAACCAGGTGTACTCGTGGCTCCTGCGC	3986
Qy	961	CTACGGCCCCCTCTCAAGGCTACCTAAGCAGCCGCTCCCCCAGGAGATGCTGCGTGCC	1020
Db	3987	CTACGGCCCCCTCTCAAGGCTACCTAAGCAGCCGCTCCCCCAGGAGATGCTGCGTGCC	4046
Qy	1021	TCAGGCCTTACCCAGAAATGGGTACAGCGTGAGATATCCAACTTCGAGTACTTGATGCAA	1080
Db	4047	TCAGGCCTTACCCAGAAATGGGTACAGCGTGAGATATCCAACTTCGAGTACTTGATGCAA	4106
Qy	1081	CTCAACACCATTGCGGGGCGGACCTACAATGACCTGTCTCAGTACCCTGTGTTCCCTGG	1140

Art Unit: 1646

Db 4107 CTCAACACCATTGCGGGGCGGACCTACAATGACCTGTCTCAGTACCCTGTGTTCCCTGG 4166

Qy 1141 GTCCTGCAGGACTACGTGTCCCAACCCTGGACCTCAGCAACCCAGCCGTCTTCCGGGAC 1200  
|||||

Db 4167 GTCCTGCAGGACTACGTGTCCCAACCCTGGACCTCAGCAACCCAGCCGTCTTCCGGGAC 4226

Qy 1201 CTGTCTAAGCCCATCGGTGTGGTGAACCCCAAGCATGCCCAGCTCGTGAGGGAGAAGTAT 1260  
|||||

Db 4227 CTGTCTAAGCCCATCGGTGTGGTGAACCCCAAGCATGCCCAGCTCGTGAGGGAGAAGTAT 4286

Qy 1261 GAAAGCTTTGAGGACCCAGCAGGGACCATTGACAAGTTCCACTATGGCACCCACTACTCC 1320  
|||||

Db 4287 GAAAGCTTTGAGGACCCAGCAGGGACCATTGACAAGTTCCACTATGGCACCCACTACTCC 4346

Qy 1321 AATGCAGCAGGCGTGATGCACTACCTCATCCGCGTGGAGCCCTTCACCTCCCTGCACGTC 1380  
|||||

Db 4347 AATGCAGCAGGCGTGATGCACTACCTCATCCGCGTGGAGCCCTTCACCTCCCTGCACGTC 4406

Qy 1381 CAGCTGCAAAGTGGCCGCTTTGACTGCTCCGACCGGCAGTTCCACTCGGTGGCGGCAGCC 1440  
|||||

Db 4407 CAGCTGCAAAGTGGCCGCTTTGACTGCTCCGACCGGCAGTTCCACTCGGTGGCGGCAGCC 4466

Qy 1441 TGGCAGGCACGCCTGGAGAGCCCTGCCGATGTGAAGGAGCTCATCCCGGAATTCTTCTAC 1500  
|||||

Db 4467 TGGCAGGCACGCCTGGAGAGCCCTGCCGATGTGAAGGAGCTCATCCCGGAATTCTTCTAC 4526

Qy 1501 TTTCTGACTTCCTGGAGAACCAGAACGGTTTGTGACCTGGGCTGTCTCCAGCTGACCAAC 1560  
|||||

Db 4527 TTTCTGACTTCCTGGAGAACCAGAACGGTTTGTGACCTGGGCTGTCTCCAGCTGACCAAC 4586

Qy 1561 GAGAAGGTAGGCGATGTGGTGCTACCCCGTGGGCCAGCTCTCCTGAGGACTTCATCCAG 1620  
|||||

Db 4587 GAGAAGGTAGGCGATGTGGTGCTACCCCGTGGGCCAGCTCTCCTGAGGACTTCATCCAG 4646

Qy 1621 CAGCACCGCCAGGCTCTGGAGTCGGAGTATGTGTCTGCACACCTACACGAGTGATCGAC 1680  
|||||

Db 4647 CAGCACCGCCAGGCTCTGGAGTCGGAGTATGTGTCTGCACACCTACACGAGTGATCGAC 4706

Qy 1681 CTCATCTTTGGCTACAAGCAGCGGGGGCCAGCCGCCGAGGAGGCCCTCAATGTCTTCTAT 1740  
|||||

Db 4707 CTCATCTTTGGCTACAAGCAGCGGGGGCCAGCCGCCGAGGAGGCCCTCAATGTCTTCTAT 4766

Qy 1741 TACTGCACCTATGAGGGGGCTGTAGACCTGGACCATGTGACAGATGAGCGGGAACGGAAG 1800  
|||||

Db 4767 TACTGCACCTATGAGGGGGCTGTAGACCTGGACCATGTGACAGATGAGCGGGAACGGAAG 4826

Qy 1801 GCTCTGGAGGGCATTATCAGCAACTTTGGGCAGACTCCCTGTCAGCTGCTGAAGGAGCCA 1860  
|||||

Db 4827 GCTCTGGAGGGCATTATCAGCAACTTTGGGCAGACTCCCTGTCAGCTGCTGAAGGAGCCA 4886

Qy 1861 CATCCAACCTCGGCTCTCAGCTGAGGAAGCAGCCCATCGCCTTGACGCCTGGACACTAAC 1920  
|||||

Db 4887 CATCCAACCTCGGCTCTCAGCTGAGGAAGCAGCCCATCGCCTTGACGCCTGGACACTAAC 4946

Qy	1921	TCACCTAGCATCTTCCAGCACCTGGACGAACTCAAGGCATTCTTCGCAGA-----	1970
Db	4947	TCACCTAGCATCTTCCAGCACCTGGACGAACTCAAGGCATTCTTCGCAGAGGTTGTCAGT	5006
Qy	1971	-----	1970
Db	5007	GATGGTGTACCCCTGGTGTCTAGCCCTGGTCCCCACCGGCAGCCCCACTCCTTCATCACC	5066
Qy	1971	-----GGTGACTGTGAGTGCCAGTGGGCTGCTGGGCACCCACAGC	2010
Db	5067	CAGGGTTCCCCAGACCTGTTGGTGACTGTGAGTGCCAGTGGGCTGCTGGGCACCCACAGC	5126
Qy	2011	TGGTTGCCCTATGACCGCAACATAAGCAACTACTTCAGCTTCAGCAAAGACCCCACCATG	2070
Db	5127	TGGTTGCCCTATGACCGCAACATAAGCAACTACTTCAGCTTCAGCAAAGACCCCACCATG	5186
Qy	2071	GGCAGCCACAAGACGCAGCGACTGCTGAGTGGCCCGTGGGTGCCAGGCAGTGGTGTGAGT	2130
Db	5187	GGCAGCCACAAGACGCAGCGACTGCTGAGTGGCCCGTGGGTGCCAGGCAGTGGTGTGAGT	5246
Qy	2131	GGACAAGCACTGGCAGTGGCCCCGGATGGAAAGCTGCTATTACAGCGGTGGCCACTGGGAT	2190
Db	5247	GGACAAGCACTGGCAGTGGCCCCGGATGGAAAGCTGCTATTACAGCGGTGGCCACTGGGAT	5306
Qy	2191	GGCAGCCTGCGGGTGACTGCACTACCCCGTGGCAAGCTGTTGAGCCAGCTCAGCTGCCAC	2250
Db	5307	GGCAGCCTGCGGGTGACTGCACTACCCCGTGGCAAGCTGTTGAGCCAGCTCAGCTGCCAC	5366
Qy	2251	CTTGATGTAGTAACCTGCCTTGCACTGGACACCTGTGGCATCTACCTCATCTCAGGCTCC	2310
Db	5367	CTTGATGTAGTAACCTGCCTTGCACTGGACACCTGTGGCATCTACCTCATCTCAGGCTCC	5426
Qy	2311	CGGGACACCACGTGCATGGTGTGGCGGCTCCTGCATCAGGGTGGTCTGTCACTAGGCCTG	2370
Db	5427	CGGGACACCACGTGCATGGTGTGGCGGCTCCTGCATCAGGGTGGTCTGTCACTAGGCCTG	5486
Qy	2371	GCACCAAAGCCTGTGCAGGTCCTGTATGGGCATGGGGCTGCAGTGAGCTGTGTGGCCATC	2430
Db	5487	GCACCAAAGCCTGTGCAGGTCCTGTATGGGCATGGGGCTGCAGTGAGCTGTGTGGCCATC	5546
Qy	2431	AGCACTGAACTTGACATGGCTGTGTCTGGATCTGAGGATGGAAGTGTGATCATACACACT	2490
Db	5547	AGCACTGAACTTGACATGGCTGTGTCTGGATCTGAGGATGGAAGTGTGATCATACACACT	5606
Qy	2491	GTACGCCGCGGACAGTTTGTAGCGGCACTACGGCCTCTGGGTGCCACATTCCCTGGACCT	2550
Db	5607	GTACGCCGCGGACAGTTTGTAGCGGCACTACGGCCTCTGGGTGCCACATTCCCTGGACCT	5666
Qy	2551	ATTTTCACCTGGCATTGGGGTCCGAAGGCCAGATTGTGGTACAGAGCTCAGCGTGGGAA	2610
Db	5667	ATTTTCACCTGGCATTGGGGTCCGAAGGCCAGATTGTGGTACAGAGCTCAGCGTGGGAA	5726
Qy	2611	CGTCCTGGGGCCAGGTCACCTACTCCTTGACCTGTATTTCAGTCAATGGGAAGTTGCGG	2670

Art Unit: 1646

Db 5727 CGTCCTGGGGCCCAGGTCACCTACTCCTTGACCTGTATTTCAGTCAATGGGAAGTTGCGG 5786

Qy 2671 GCTTCACTGCCCCCTGGCAGAGCAGCCTACAGCCCTGACGGTGACAGAGGACTTTGTGTTG 2730  
|||||

Db 5787 GCTTCACTGCCCCCTGGCAGAGCAGCCTACAGCCCTGACGGTGACAGAGGACTTTGTGTTG 5846

Qy 2731 CTGGGCACCGCCCAGTGCGCCCTGCACATCCTCCAATAAACACACTGCTCCCGGCCGCG 2790  
|||||

Db 5847 CTGGGCACCGCCCAGTGCGCCCTGCACATCCTCCAATAAACACACTGCTCCCGGCCGCG 5906

Qy 2791 CCTCCCTTGCCCATGAAGGTGGCCATCCGCAGCGTGGCCGTGACCAAGGAGCGCAGCCAC 2850  
|||||

Db 5907 CCTCCCTTGCCCATGAAGGTGGCCATCCGCAGCGTGGCCGTGACCAAGGAGCGCAGCCAC 5966

Qy 2851 GTGCTGGTGGGCCTGGAGGATGGCAAGCTCATCGTGGTGGTCGCGGGGCAGCCCTCTGAG 2910  
|||||

Db 5967 GTGCTGGTGGGCCTGGAGGATGGCAAGCTCATCGTGGTGGTCGCGGGGCAGCCCTCTGAG 6026

Qy 2911 GTGCGCAGCAGCCAGTTTCGCGCGGAAGCTGTGGCGGTCCTCGCGGCGCATCTCCCAGGTG 2970  
|||||

Db 6027 GTGCGCAGCAGCCAGTTTCGCGCGGAAGCTGTGGCGGTCCTCGCGGCGCATCTCCCAGGTG 6086

Qy 2971 TCCTCGGGAGAGACGGAATACAACCCTACTGAGGCGCGC 3009  
|||||

Db 6087 TCCTCGGGAGAGACGGAATACAACCCTACTGAGGCGCGC 6125

Art Unit: 1646

; Sequence 827, Application US/09023655  
; Patent No. 6607879  
; GENERAL INFORMATION:  
; APPLICANT: Cocks, Benjamin G.  
; INFORMATION FOR SEQ ID NO: 827:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1595 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: LUNGAST01  
; CLONE: 873034  
US-09-023-655-827

Query Match 38.7%; Score 1367.2; DB 4; Length 1595;  
Best Local Similarity 93.6%; Pred. No. 4.2e-304;  
Matches 1494; Conservative 0; Mismatches 10; Indels 92; Gaps 3;

Qy	1807	GGAGAACCAGAACGGTTTTGACCTGGGCTGTCTCCAGCTGACCAACGAGAAGGTAGGCGA	1866
Db	1	GGAGAACCAGAACGGTTTTGACCTGGGCTGTCTCCAGCTGACCAACGAGAAGGTAGGCGA	60
Qy	1867	TGTGGTGCTACCCCCGTGGGCCAGCTCTCCTGAGGACTTCATCCAGCAGCACCGCCAGGC	1926
Db	61	TGTGGTGCTACCCCCGTGGGCCAGCTCTCCTGAGGACTTCATCCAGCAGCACCGCCAGGC	120
Qy	1927	TCTGGAGTCGGAGTATGTGTCTGCACACCTACACGAGTGGATCGACCTCATCTTTGGCTA	1986
Db	121	TCTGGAGTCGGAGTATGTGTCTGCACANCTACACGAGTGGATCGACCTCATCTTTGGNTA	180
Qy	1987	CAAGCAGCGGGGGCCAGCCGCCGAGGAGGCCCTCAATGTCTTCTATTACTGCACCTATGA	2046
Db	181	TAAGCAGCGGGGGCCAGCCGCCGAGGAGGCCCTCAATGTCTTCTATTACTGCACCTATGA	240
Qy	2047	GGGGGCTGTAGACCTGGACCATGTGACAGATGAGCGGGAACGGAAGGCTCTGGAGGGCAT	2106
Db	241	GGGGGCTGTAGACCTGGACCATGTGACAGATGAGCGGGAACGGAAGGCTCTGGAGGGCAT	300
Qy	2107	TATCAGCAACTTTGGGCAGACTCCCTGTGCTGCTGAAGGAGCCACATCCAACCTCGGCT	2166
Db	301	TATCAGCAACTTTGGGCAGACTCCCTGTGCTGCTGAAGGAGCCACATCCAACCTCGGCT	360
Qy	2167	CTCAGCTGAGGAAGCAGCCCATCGCCTTGACGCTGGACACTAACTCACCTAGCATCTT	2226
Db	361	CTCAGCTGAGGAAGCAGCCCATCGCCTTGACGCTGGACACTAACTCACCTAGCATCTT	420
Qy	2227	CCAGCACCTGGACGAACTCAAGGCATTCTTCGCAGA-----	2262
Db	421	CCAGCACCTGGACGAACTCAAGGCATTCTTCGCAGAGGTTGTCAGTGATGGTGTACCCCT	480
Qy	2263	-----	2262
Db	481	GGTGCTAGCCCTGGTCCCCCACCAGGAGCCCCACTCCTTCATCACCCAGGGTCCCCAGA	540

Art Unit: 1646

Qy 2263 -----GGTGACTGTGAGTGCCAGTGGGCTGCTGGGCACCCACAGCT-GGTTGCCCTATG 2315  
|||  
Db 541 CCTGTTGGTGACTGTGAGTGCCAGTGGGCTGCTGGGCACCCACAGCTGGGTTGCCCTATG 600

Qy 2316 ACCGCAACATAAGCAACTACTTCAGCTTCAGCAAAGACCCACCATGGGCAGCCACAAGA 2375  
|||  
Db 601 ACCGCAACATAAGCAACTACTTCAGCTTCAGCAAAGACCCACCATGGGCAGCCACAAGA 660

Qy 2376 CGCAGCGACTGCTGAGTGGCCCGTGGGTGCCAGGCAGTGGTGTGAGTGGACAAGCACTGG 2435  
|||  
Db 661 CGCAGCGACTGCTGAGTGGCCCGTGGGTGCCAGGCAGTGGTGTGAGTGGACAAGCACTGG 720

Qy 2436 CAGTGGCCCCGGATGGAAAGCTGCTATTTCAGCGGTGGCCACTGGGATGGCAGCCTGCGGG 2495  
|||  
Db 721 CAGTGGCCCCGGATGGAAAGCTGCTATTTCAGCGGTGGCCACTGGGATGGCAGCCTGCGGG 780

Qy 2496 TGA CTGCACTACCCCGTGGCAAGCTGTTGAGCCAGCTCAGCTGCCACCTTGATGTAGTAA 2555  
|||  
Db 781 TGA CTGCACTACCCCGTGGCAAGCTGTTGAGCCAGCTCAGCTGCCACCTTGATGTAGTAA 840

Qy 2556 CCTGCCTTGCACTGGACACCTGTGGCATCTACCTCATCTCAGGCTCCCGGGACACCACGT 2615  
|||  
Db 841 CCTGCCTTGCACTGGACACCTGTGGCATCTACCTCATCTCAGGCTCCCGGGACACCACGT 900

Qy 2616 GCATGGTGTGGCGGCTCCTGCATCAGGGTGGTCTGTGTCAGTAGGCCTGGCACCAAAGCCTG 2675  
|||  
Db 901 GCATGGTGTGGCGGCTCCTGCATCAGGGTGGTCTGTGTCAGTAGGCCTGGCACCAAAGCCTG 960

Qy 2676 TGCAGGTCCTGTATGGGCATGGGGCTGCAGTGAGCTGTGTGGCCATCAGCACTGAACTTG 2735  
|||  
Db 961 TGCAGGTCCTGTATGGGCATGGGGCTGCAGTGAGCTGTGTGGCCATCAGCACTGAACTTG 1020

Qy 2736 ACATGGCTGTGTCTGGATCTGAGGATGGAAGTGTGATCATAACACTGTACGCCGCGGAC 2795  
|||  
Db 1021 ACATGGCTGTGTCTGGATCTGAGGATGGAAGTGTGATCATAACACTGTACGCCGCGGAC 1080

Qy 2796 AGTTTGTAGCGGCACTACGGCCTCTGGGTGCCACATTCCCTGGACCTATTTTCCACCTGG 2855  
|||  
Db 1081 AGTTTGTAGCGGCACTACGGCCTCTGGGTGCCACATTCCCTGGACCTATTTTCCACCTGG 1140

Qy 2856 CATTGGGGTCCGAAGGCCAGATTGTGGTACAGAGCTCAGCGTGGGAACGTCTTGGGGCCC 2915  
|||  
Db 1141 CATTGGGGTCCGAATGCCAGATTGTGGTACAGAGCTCAGCGTGGGAACGTCTTGGGGCCC 1200

Qy 2916 AGGTCACCTACTCCTTGACCTGTATTTCAGTCAATGGGAAGTTGCGGGCTTCACTGCCCC 2975  
|||  
Db 1201 AGGTCACCTACTCCTTGACCTGTATTTCAGTCAATGGGAAGTTGCGGGCTTCACTGCCCC 1260

Qy 2976 TGGCAGAGCAGCCTACAGCCCTGACGGTGACAGAGGACTTTGTGTTGCTGGGCACCGCCC 3035  
|||  
Db 1261 TGGCAGAGCAGCCTACAGCCCTGACGGTGACAGAGGACTTTGTGTTGCTGGGCACCGCCC 1320

Qy 3036 AGTGCGCCCTGCACATCTCCAATAAACACACTGCTCCCGGCCGCGCCTCCCTTGCCCA 3095

Db	1321	AGTGCGCCCTGCACATCCTCCAACATAACACACTGCTCCCGGCCGCGCCTCCCTTGCCCCA	1380
Qy	3096	TGAAGGTGGCCATCCGCAGCGTGGCCGTGACCAAGGAGCGCAGCCACGTGCTGGTGGGCC	3155
Db	1381	TGAAGGTGGCCATCCGCAGCGTGGCCGTGACCAAGGAGCGCA-CCACGTGCTGGTGGGCC	1439
Qy	3156	TGGAGGATGGCAAGCTCATCGTGGTGGTCGCGGGGCAGCCCTCTGAGGTGCGCAGCAGCC	3215
Db	1440	TGGAGGATGGCAAGCTCATCGTGGTGGTCGCGGGGCAGCCCTCTGAGGTGCGCACAGCCC	1499
Qy	3216	AGTTCGCGCGGAAGCTGTGGCGGTCCCTCGCGGCGCATCTCCCAGGTGTCCTCGGGAGAGA	3275
Db	1500	AGTTCGCGCGGAAGCTGTGGCGGTCCCTCGCGGCGCATCTCCCAGGTGTCCTCGGGAGAGA	1559
Qy	3276	CGGAATACAACCCCTACTGAGGCGCGCTGAACCTGGC	3311
Db	1560	CGGAATACAACCCCTACTGAGGCGCGCTGAACCTGGC	1595

Art Unit: 1646

## Coding only

; Sequence 827, Application US/09023655

; Patent No. 6607879

; GENERAL INFORMATION:

; APPLICANT: Cocks, Benjamin G.

; INFORMATION FOR SEQ ID NO: 827:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1595 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; IMMEDIATE SOURCE:

; LIBRARY: LUNGAST01

; CLONE: 873034

US-09-023-655-827

Query Match 45.1%; Score 1357.2; DB 4; Length 1595;  
Best Local Similarity 93.6%; Pred. No. 6.9e-308;  
Matches 1484; Conservative 0; Mismatches 10; Indels 92; Gaps 3;

```
Qy      1515 GGAGAACCGAACCGTTTTGACCTGGGCTGTCTCCAGCTGACCAACGAGAAGGTAGGCGA 1574
          |||
Db      1   GGAGAACCGAACCGTTTTGACCTGGGCTGTCTCCAGCTGACCAACGAGAAGGTAGGCGA 60

Qy      1575 TGTGGTGCTACCCCCGTGGGCCAGCTCTCCTGAGGACTTCATCCAGCAGCACCCGCCAGGC 1634
          |||
Db      61   TGTGGTGCTACCCCCGTGGGCCAGCTCTCCTGAGGACTTCATCCAGCAGCACCCGCCAGGC 120

Qy      1635 TCTGGAGTCGGAGTATGTGTCTGCACACCTACACGAGTGGATCGACCTCATCTTTGGCTA 1694
          |||
Db      121  TCTGGAGTCGGAGTATGTGTCTGCACANCTACACGAGTGGATCGACCTCATCTTTGGNTA 180

Qy      1695 CAAGCAGCGGGGGCCAGCCGCCGAGGAGGCCCTCAATGTCTTCTATTACTGCACCTATGA 1754
          |||
Db      181  TAAGCAGCGGGGGCCAGCCGCCGAGGAGGCCCTCAATGTCTTCTATTACTGCACCTATGA 240

Qy      1755 GGGGGCTGTAGACCTGGACCATGTGACAGATGAGCGGGAACGGAAGGCTCTGGAGGGCAT 1814
          |||
Db      241  GGGGGCTGTAGACCTGGACCATGTGACAGATGAGCGGGAACGGAAGGCTCTGGAGGGCAT 300

Qy      1815 TATCAGCAACTTTGGGCAGACTCCCTGTCTAGCTGCTGAAGGAGCCACATCCAACCTCGGCT 1874
          |||
Db      301  TATCAGCAACTTTGGGCAGACTCCCTGTCTAGCTGCTGAAGGAGCCACATCCAACCTCGGCT 360

Qy      1875 CTCAGCTGAGGAAGCAGCCCATCGCCTTGACGCCTGGACACTAACTCACCTAGCATCTT 1934
          |||
Db      361  CTCAGCTGAGGAAGCAGCCCATCGCCTTGACGCCTGGACACTAACTCACCTAGCATCTT 420

Qy      1935 CCAGCACCTGGACGAACTCAAGGCATTCTTCGCAGA----- 1970
          |||
Db      421  CCAGCACCTGGACGAACTCAAGGCATTCTTCGCAGAGGTTGTCAGTGATGGTGTACCCCT 480

Qy      1971 ----- 1970
```



Art Unit: 1646

Db 481 GGTGCTAGCCCTGGTCCCCCACCAGCAGCCCCACTCCTTCATCACCAGGGTTCCCCAGA 540

Qy 1971 -----GGTGA CTGTGAGTGCCAGTGGGCTGCTGGGCACCCACAGCT-GGTTGCCCTATG 2023  
|||||

Db 541 CCTGTTGGTGA CTGTGAGTGCCAGTGGGCTGCTGGGCACCCACAGCTGGGTTGCCCTATG 600

Qy 2024 ACCGCAACATAAGCAACTACTTCAGCTTCAGCAAAGACCCACCATGGGCAGCCACAAGA 2083  
|||||

Db 601 ACCGCAACATAAGCAACTACTTCAGCTTCAGCAAAGACCCACCATGGGCAGCCACAAGA 660

Qy 2084 CGCAGCGACTGCTGAGTGGCCCGTGGGTGCCAGGCAGTGGTGTGAGTGGACAAGCACTGG 2143  
|||||

Db 661 CGCAGCGACTGCTGAGTGGCCCGTGGGTGCCAGGCAGTGGTGTGAGTGGACAAGCACTGG 720

Qy 2144 CAGTGGCCCCGGATGGAAAGCTGCTATTTCAGCGGTGGCCACTGGGATGGCAGCCTGCGGG 2203  
|||||

Db 721 CAGTGGCCCCGGATGGAAAGCTGCTATTTCAGCGGTGGCCACTGGGATGGCAGCCTGCGGG 780

Qy 2204 TGA CTGCACTACCCCGTGGCAAGCTGTTGAGCCAGCTCAGCTGCCACCTTGATGTAGTAA 2263  
|||||

Db 781 TGA CTGCACTACCCCGTGGCAAGCTGTTGAGCCAGCTCAGCTGCCACCTTGATGTAGTAA 840

Qy 2264 CCTGCCTTGCACTGGACACCTGTGGCATCTACCTCATCTCAGGCTCCCGGGACACCACGT 2323  
|||||

Db 841 CCTGCCTTGCACTGGACACCTGTGGCATCTACCTCATCTCAGGCTCCCGGGACACCACGT 900

Qy 2324 GCATGGTGTGGCGGCTCCTGCATCAGGGTGGTCTGTGTCAGTAGGCCTGGCACCAAAGCCTG 2383  
|||||

Db 901 GCATGGTGTGGCGGCTCCTGCATCAGGGTGGTCTGTGTCAGTAGGCCTGGCACCAAAGCCTG 960

Qy 2384 TGCAGGTCCTGTATGGGCATGGGGCTGCAGTGAGCTGTGTGGCCATCAGCACTGAACTTG 2443  
|||||

Db 961 TGCAGGTCCTGTATGGGCATGGGGCTGCAGTGAGCTGTGTGGCCATCAGCACTGAACTTG 1020

Qy 2444 ACATGGCTGTGTCTGGATCTGAGGATGGAAGTGTGATCATACACTGTACGCCGCGGAC 2503  
|||||

Db 1021 ACATGGCTGTGTCTGGATCTGAGGATGGAAGTGTGATCATACACTGTACGCCGCGGAC 1080

Qy 2504 AGTTTGTAGCGGCACTACGGCCTCTGGGTGCCACATTCCCTGGACCTATTTTCCACCTGG 2563  
|||||

Db 1081 AGTTTGTAGCGGCACTACGGCCTCTGGGTGCCACATTCCCTGGACCTATTTTCCACCTGG 1140

Qy 2564 CATTGGGGTCCGAAGGCCAGATTGTGGTACAGAGCTCAGCGTGGGAACGTCCTGGGGCCC 2623  
|||||

Db 1141 CATTGGGGTCCGAATGCCAGATTGTGGTACAGAGCTCAGCGTGGGAACGTCCTGGGGCCC 1200

Qy 2624 AGGTCACCTACTCCTTGACCTGTATTTCAGTCAATGGGAAGTTGCGGGCTTCACTGCCCC 2683  
|||||

Db 1201 AGGTCACCTACTCCTTGACCTGTATTTCAGTCAATGGGAAGTTGCGGGCTTCACTGCCCC 1260

Qy 2684 TGGCAGAGCAGCCTACAGCCCTGACGGTGACAGAGGACTTTGTGTTGCTGGGCACCGCCC 2743  
|||||

Db 1261 TGGCAGAGCAGCCTACAGCCCTGACGGTGACAGAGGACTTTGTGTTGCTGGGCACCGCCC 1320

Art Unit: 1646

Qy	2744	AGTGCGCCCTGCACATCCTCCAATAAACACACTGCTCCCGGCCGCGCCTCCCTTGCCCA	2803
Db	1321	AGTGCGCCCTGCACATCCTCCAATAAACACACTGCTCCCGGCCGCGCCTCCCTTGCCCA	1380
Qy	2804	TGAAGGTGGCCATCCGCAGCGTGGCCGTGACCAAGGAGCGCAGCCACGTGCTGGTGGGCC	2863
Db	1381	TGAAGGTGGCCATCCGCAGCGTGGCCGTGACCAAGGAGCGCA-CCACGTGCTGGTGGGCC	1439
Qy	2864	TGGAGGATGGCAAGCTCATCGTGGTGGTTCGCGGGGCAGCCCTCTGAGGTGCGCAGCAGCC	2923
Db	1440	TGGAGGATGGCAAGCTCATCGTGGTGGTTCGCGGGGCAGCCCTCTGAGGTGCGCACAGCCC	1499
Qy	2924	AGTTCGCGCGGAAGCTGTGGCGGTCCCTCGCGGCGCATCTCCCAGGTGTCCTCGGGAGAGA	2983
Db	1500	AGTTCGCGCGGAAGCTGTGGCGGTCCCTCGCGGCGCATCTCCCAGGTGTCCTCGGGAGAGA	1559
Qy	2984	CGGAATACAACCCTACTGAGGCGCGC	3009
Db	1560	CGGAATACAACCCTACTGAGGCGCGC	1585

Art Unit: 1646

hypothetical protein KIAA0540 - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 01-Feb-1999 #sequence\_revision 01-Feb-1999 #text\_change 11-Jan-2002

C;Accession: T00271

R;Nagase, T.; Ishikawa, K.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.

DNA Res. 5, 31-39, 1998

A;Title: Prediction of the coding sequences of unidentified human genes. IX. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro.

A;Reference number: Z14086; MUID:98290545; PMID:9628581

A;Accession: T00271

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-1113 &lt;NAG&gt;

A;Cross-references: EMBL:AB011112; NID:d1185382; PIDN:BAA25466.1

A;Experimental source: brain

C;Genetics:

A;Note: KIAA0540

Query Match 34.3%; Score 1802; DB 2; Length 1113;  
Best Local Similarity 100.0%; Pred. No. 4.3e-121;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MSQFEMDTYAKSHDLMSGFWNACYDMLMSSGQRRQWERAQSRRAFQELVLEPAQRRARLE 60
      |||
Db      756 MSQFEMDTYAKSHDLMSGFWNACYDMLMSSGQRRQWERAQSRRAFQELVLEPAQRRARLE 815

Qy      61 GLRYTAVLKQQATQHSMALLHWGALWRQLASPCGAWALRDTPIPRWKLSSAETYSRMRLE 120
      |||
Db      816 GLRYTAVLKQQATQHSMALLHWGALWRQLASPCGAWALRDTPIPRWKLSSAETYSRMRLE 875

Qy      121 LVPNHHFDPHLEASALRDNLGEVPLTPTEEASLPLAVTKEAKVSTPPELLQEDQLGEDEL 180
      |||
Db      876 LVPNHHFDPHLEASALRDNLGEVPLTPTEEASLPLAVTKEAKVSTPPELLQEDQLGEDEL 935

Qy      181 AELETPMEAAELDEQREKLVLSAECQLVTVVAVVPGLLEVTTQNVYFYDGSTERVETEEG 240
      |||
Db      936 AELETPMEAAELDEQREKLVLSAECQLVTVVAVVPGLLEVTTQNVYFYDGSTERVETEEG 995

Qy      241 IGYDFRRPLAQLREVHLRRFNLRRSALELFFIDQANYFLNFPCKVGTTPVSSPSQTPRPQ 300
      |||
Db      996 IGYDFRRPLAQLREVHLRRFNLRRSALELFFIDQANYFLNFPCKVGTTPVSSPSQTPRPQ 1055

Qy      301 PGPIPPHTQVRNQVYSWLLRLRPPSQGYLSSRSPQEMLRASGLTQ 345
      |||
Db     1056 PGPIPPHTQVRNQVYSWLLRLRPPSQGYLSSRSPQEMLRASGLTQ 1100
```